

AMENDMENTS TO THE SPECIFICATION

Insert the attached sheet entitled "Abstract" after the claims as page number 50.

Insert the Sequence Listing as separately numbered pages 1 - 86 after the abstract.

Replace the paragraph beginning at page 6, line 4 with the following amended paragraph:

Figure 3. (a) ~~The~~ The amino acid sequence of IL-6R extracellular domain **(SEQ ID No: 83)**, showing the CBD comprising domain D2 (residues 92 to 195) and domain D3 (residues 196 to 297). The position of β -sheet structures are indicated by #. The position of loops in the cytokine binding region are shown by * and marked L1 to L7. The Pro94, Pro95, Cys102, Cys103, Trp115, Cys146, Cys157, Pro199, Pro200, Trp219, Arg274, Trp284, Ser285, Trp287 and Ser288 residues are all conserved in known CBDs. The Leu100, Leu108, Val111, Ala127, Leu129, Val131, Leu159, Tyr169, Val171, Met173, Val175, Phe189, Gly191, Ile194, Leu195, Pro197, Ile203, Val205, Leu215, Val217, Leu232, Phe234, Leu236, Tyr238, Phe246, Trp249, Ile260, Ala263, Val271, Leu273, and Glu286 residues are mainly conserved hydrophobic residues in known CBDs. The Pro98, Pro117, Trp225, Cys258, His269, Ala291 and Gly293 are, in the majority, conserved residues in all known CBDs.

Replace the paragraph beginning at page 6, line 16 with the following amended paragraph:

Figure 3(b) Figure 3A depicts the sequence alignment of the CBDs from IL-6R, IL-11R, PRLR and GCSR. Loops L1 to L7 are outlined by boxes.

Replace the paragraph beginning at page 6, line 23 with the following amended paragraph:

Figure 5. Comparison of the sequences of CBDs from a number of known 77
~~known~~ genes (SEQ ID Nos:1-82). Figure 5A compares the sequences in the "first" FnIII
 domain, containing loops 1 to 4, and Figure 5B the sequences in the "second" FnIII
 domain, containing the loops 5-7. Conserved residues as described in Example 3 for the
 IL-6 receptor are aligned according to their sequence homologies. For example the
 hydrophobic residues, the cysteine residues (C) and in some cases two prolines side by
 side (PP) are aligned. The location of the 7 binding loops is indicated by the double-
 headed arrows..

Replace the paragraph beginning at page 35, line 16 with the following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and
 Cys258 in bold) is shown below as sequence (a). The corresponding partial DNA
 sequence of the D3 library clone, showing changes in loop 6 and at Cys258 (mutated to
 Ser) shown as sequence (b).

(a) R S K T F T T W **M V K D L** Q H H **C** V I H D A W S G L R H
 (b) R S K T F T T W **A Q S R W** Q H H **S** V I H D A W S G L R H

(a) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:84)
 (b) V V Q L R A **Q E E F G Q G** E W S E W (SEQ ID No:85)

Replace the paragraph beginning at page 35, line 32 (and ending at page 36, line 2) with the
 following amended paragraph:

The partial DNA sequence of IL-6R D3 (loops 6 and 7 in bold and boxed, and
 Cys258 in bold) is shown below as sequence (c). The corresponding partial DNA

sequence of the D3 library clone, showing changes in loops 6 and 7 and at Cys258
(mutated to Ser) shown as sequence (d).

(c) R S K T F T T W M V K D L Q H H C V I H D A W S G L R H
(d) R S K T F T T W S R Q N D Q H H S V I H D A W S G L R H

(c) V V Q L R A Q E E F G Q G E W S E W (SEQ ID No:86)
(d) V V Q L R A R N E V R V G E W S E W (SEQ ID No:87)

Replace the paragraph beginning at page 37, line 3 with the following amended paragraph:

The CBD of human prolactin receptor has the following amino acid sequence
(SEQ ID No:21):

```
24      GQLPPGK PEIFKCRSPN KETFTCWWRP GTDGGGLPTNY
                                L1
61      SLTYHREGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI
                                L2                                L3
101     MMVNATNQMG SSFSDELYVD VTYIVQPDPP LELAVEVKQP
                                L4
141     EDRKPYLWIK WSPPTLIDLK TGWFTLLYEI RLKPEKAAEW
                                L5
181     EIHFAGQQTE FKILSLHPGQ KYLVQVRCKP DHGYWSAWSP
                                L6                                L7
221     ATFIQIPSD 229
```

The first FnIII-like domain is defined by amino acids Glu24 to Val125 and the second
Fn-III like domain by Gln126 to Asp229. Loops L1 to L7 are indicated as boxed residues
on the above sequence.

Replace the paragraph beginning at page 38, line 3 with the following amended paragraph:

The CBD of IL-11R has the following amino acid sequence (SEQ ID No:27):

```
111  YPPARPVVSC QAAADYENFSC TWSPSQISGL PTRYLTSYRK
                        L1
151  KTVLGADSQR RS PSTGPWPC PQDPLGAARC VVHGAEFWSQ
                        L2                                L3
191  YRINVTEVNP LGASTRLLDV SLQSI LR PDP PQGLRVESVP
                        L4
231  GYPRRLRASW TYPASWP CQP HFL LK FRLQY RPAQHPAWST
                        L5
271  VEPAGLEEV I TDAVAGLPHA VRVSA R DFLD AGTWSTWSPE
                        L6                                L7
321  AWGTPSTGT 329
321  AWGTPSTG 328
```

The first FnIII-like domain is defined by amino acids 112-214 and the second FnIII-like domain by amino acids 218-318. Loops L1 to L7 are indicated as boxed residues on the above sequence.

Replace the paragraph beginning at page 38, line 31 with the following amended paragraph:

The first FnIII-like domain derived from the CBD of prolactin receptor is defined by residues 24-125 ~~[IS THIS CORRECT—see Ex 9 questions]~~ as in Example 9.

Replace the paragraph beginning at page 38, line 34 (and ending on page 39, line 8) with the following amended paragraph:

The CBD of GSCFR has the following amino acid sequence (SEQ ID No:2):

```
121  YPPAIPHNLS CLMNLTSSL ICQWEPGPET HLPTSFTLKS
                        L1
161  FKSRGNCQTQ GDSILDCVPK DGQSHCCIPR KHLLLYQNMG
                        L2                        L3
201  IWVQAENALG TSMSPQLCLDPMDVVKLEPP MLRTMDPSPE
                        L4
241  AAPQAGCLQ LCWEPWQPGL HINQKCELRH KPQGEASWA
                        L5
281  LVGPLPLEAL QYELCGLLPA TAYTLQIRCIRWPLPGHWSD
                        L6                        L7
321  WSPSLELRTT ERA 333
```

Loops L1 to L7 of the CBD of GCSFR are indicated as boxed residues on the above sequence. The second region of the CBD of GCSFR is defined by residues 237-330.